



Figure 1A

Query = C54D2.5 CE02562 CALCIUM CHANNEL ALPHA-1 SUBUNIT LG:6

Database: Non-redundant Database of GenBank EST Division

824,500 sequences; 302,742,428 total letters.

H55225 CHR220164 Homo sapiens genomic clone C22_207 5'.

Length = 168

Plus Strand HSPs:

Score = 136 (63.8 bits), Expect = 2.5e-10, P = 2.5e-10

Identities = 23/31 (74%), Positives = 29/31 (93%), Frame = +1

Query: 440 VISLEGWTDIMYYVQDAHSFVNWIYFVLLIV 470 SEQ ID NO. 24

VI LEGW IMYYV DAHSF N IYF LLI

Sbjct: 1 VITLEGWVEIMYYVMDAHSFYNFYIFILLII 93 SEQ ID NO. 25

H55617 CHR220556 Homo sapiens genomic clone C22_757 5'.

Length = 98

Plus Strand HSPs:

Score = 102 (47.9 bits), Expect = 2.8e-05, P = 2.8e-05

Identities = 19/23 (82%), Positives = 23/23 (100%), Frame = +2

Query: 243 NINLTAIRTVRVLRPLRAVNRIP 265 SEQ ID NO. 26

NINL AIRTVRVLRPL A NR P

Sbjct: 29 NINLSAIRTVRVLRPLKAINRVP 97 SEQ ID NO. 27

H55223 CHR220162 Homo sapiens genomic clone C22_204 5'.

Length = 94

Plus Strand HSPs:

Score = 87 (40.8 bits), Expect = 0.0039, P = 0.0039

Identities = 14/19 (73%), Positives = 18/19 (94%), Frame = +2

Query: 154 MAVIMINCVTLGMYRPCED 172 SEQ ID NO. 28

M VI NCVTLGMY PC D

Sbjct: 2 MLVILLNCVTLGMYQPCDD 58 SEQ ID NO. 29



Figure 1B

H55544 CHR220483 Homo sapiens genomic clone C22_651 5'

Length = 123

Plus Strand HSPs:

Score = 65 (30.5 bits), Expect = 3.8, P = 0.98

Identities = 12/23 (52%), Positives = 18/23 (78%), Frame = +1

Query: 246 LTAIRTVRVLRPLRAVNRIPSMR 268 SEQ ID NO. 30

RT R LRPLRA R MR

Sbjct: 55 IKSLRTLRLALRPLRALSRLFEGMR 123 SEQ ID NO. 31

F07776| HSC2HD061 H. sapiens partial cDNA sequence; clone c-2hd06

Length = 343

Plus Strand HSPs:

Score = 100 (46.9 bits), Expect = 0.00057, P = 0.00057

Identities = 21/41 (51%), Positives = 31/41 (75%), Frame = +3

Query: 1480 PTIIRVMRVLRIARVLKLLKMAKGIRSLDDTVGEALPQVGN 1520 SEQ ID NO. 32

PT+ RV+R+ RI R+L+L+K AKGIR+LL + +LP + N

Sbjct: 57 PTLXRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFN 179 SEQ ID NO. 33